

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input checked="" type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response. <i>47-9</i>	
12 <input checked="" type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

Never

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/424,487A

DATE: 03/28/2001
 TIME: 15:24:58

Input Set : N:\Crf3\Refhold\I424487A.raw
 Output Set: N:\CRF3\03282001\I424487A.raw

Does Not Comply
 Corrected Diskette Needed

1 <110> APPLICANT: CHOO, Yen
 2 KLUG, Aaron
 3 ISALAN, Mark
 4 <120> TITLE OF INVENTION: Nucleic Acid Binding Proteins
 5 <130> FILE REFERENCE: 71278/264975
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/424,487A
 7 <141> CURRENT FILING DATE: 2000-02-29
 8 <150> PRIOR APPLICATION NUMBER: GB 9710809.6
 9 <151> PRIOR FILING DATE: 1997-05-23
 10 <150> PRIOR APPLICATION NUMBER: PCT/GB98/01512
 11 <151> PRIOR FILING DATE: 1998-05-26
 12 <160> NUMBER OF SEQ ID NOS: 17
 13 <170> SOFTWARE: PatentIn Ver. 2.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 264
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Artificial Sequence
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (1)..(264)
 22 <223> OTHER INFORMATION: Description of Artificial Sequence: encoding
 nucleic acid binding proteins
 24 <400> SEQUENCE: 1
 25 gca gaa gag aag cct ttt cag tgt cga atc tgc atg cgt aac ttc agc 48
 26 Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
 27 1 5 10 15
 28 gat cgt act act ctt acc cgc cac acg agg acc cac aca ggc gag aag 96
 29 Asp Arg Thr Thr Leu Thr Arg His Thr Arg Thr Gly Glu Lys
 30 20 25 30
 31 cct ttt cag tgt cga atc tgc atg cgt aac ttc agc agg agc gat aac 144
 32 Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn
 33 35 40 45
 34 ctt acg aga cac cta agg acc cac aca ggc gag aag cct ttt cag tgt 192
 35 Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys
 36 50 55 60
 37 cga atc tgc atg cgt aac ttc agg caa gct gat cat ctt caa gag cac 240
 38 Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His
 39 65 70 75 80
 40 cta aag acc cac aca ggc gag aag
 41 Leu Lys Thr His Thr Gly Glu Lys
 42 85
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 88
 46 <212> TYPE: PRT
 47 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <223> OTHER INFORMATION: Description of Artificial Sequence: encoding

JPR 2-4

RAW SEQUENCE LISTING
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50      nucleic acid binding proteins
51 <400> SEQUENCE: 2
52      Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
53          1           5           10           15
54      Asp Arg Thr Thr Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
55          20          25           30
56      Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn
57          35          40           45
58      Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys
59          50          55           60
60      Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His
61          65          70           75           80
62      Leu Lys Thr His Thr Gly Glu Lys
63          85

65 <210> SEQ ID NO: 3
66 <211> LENGTH: 18
67 <212> TYPE: PRT
68 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
71      binding protein
72 <221> NAME/KEY: BINDING
73 <222> LOCATION: (1)..(18)
74 <223> OTHER INFORMATION: where X is any amino acid
75 <400> SEQUENCE: 3
W--> 76      Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa
77          1           5           10           15
W--> 78      Xaa His
80 <210> SEQ ID NO: 4
81 <211> LENGTH: 21
82 <212> TYPE: PRT
83 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Description of Artificial Sequence: where X is any
86      amino acid
87 <221> NAME/KEY: BINDING
88 <222> LOCATION: (1)..(21)
89 <400> SEQUENCE: 4
W--> 90      Xaa Cys Xaa Xaa Cys Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
91          1           5           10           15
W--> 92      His Xaa Xaa Xaa His
93          20

95 <210> SEQ ID NO: 5
96 <211> LENGTH: 26
97 <212> TYPE: PRT
98 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus zinc
101      finger structure

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This does not describe
the genetic
source
of Artificial
Sequence.
See item 12 on
Error Summary
Sheet.

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102 <221> NAME/KEY: BINDING
103 <222> LOCATION: (1)..(26)
104 <400> SEQUENCE: 5
105     Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Lys Ser Asp
106         1           5           10          15
107     Leu Val Lys His Gln Arg Thr His Thr Gly
108             20          25
110 <210> SEQ ID NO: 6
111 <211> LENGTH: 29
112 <212> TYPE: PRT
113 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
116     zinc finger structure
117 <221> NAME/KEY: BINDING
118 <222> LOCATION: (1)..(29)
119 <400> SEQUENCE: 6
120     Pro Tyr Lys Cys Ser Glu Cys Gly Lys Ala Phe Ser Gln Lys Ser Asn
121         1           5           10          15
122     Leu Thr Arg His Gln Arg Ile His Thr Gly Glu Lys Pro
123             20          25
125 <210> SEQ ID NO: 7
126 <211> LENGTH: 9
127 <212> TYPE: PRT
128 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: where x
131     denotes a given combination of the bases at
132     interface between DNA subsites, and the four bases
133     are equally represented at DNA position 3
134 <221> NAME/KEY: BINDING
135 <222> LOCATION: (1)..(9)
136 <400> SEQUENCE: 7
W--> 137     Gly Asn Xaa Xaa Cys Gly Gly Cys Gly
138         1           5
140 <210> SEQ ID NO: 8
141 <211> LENGTH: 9
142 <212> TYPE: PRT
143 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Description of Artificial Sequence: where x
146     denotes a known combination of the two bases at
147     DNA positions 4X and 5X and there is equal
148     probability of any of the four bases at DNA position 3
149 <221> NAME/KEY: BINDING
150 <222> LOCATION: (1)..(9)
151 <400> SEQUENCE: 8
W--> 152     Gly Asn Xaa Xaa Cys Gly Gly Cys Gly
153         1           5

```

1) This statement does not explain Artificial Sequence;
 2) Xaa can only be a single amino acid, not a base.

same error

RAW SEQUENCE LISTING
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TIME: 15:24:58

Input Set : N:\Crf3\Refhold\I424487A.raw
Output Set: N:\CRF3\03282001\I424487A.raw

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155 <210> SEQ ID NO: 9
156 <211> LENGTH: 9
157 <212> TYPE: PRT
158 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence: where X
161     denotes a known combination of the two bases at
162     DNA positions 4X and 5X
163 <221> NAME/KEY: BINDING
164 <222> LOCATION: (1)..(9)
165 <400> SEQUENCE: 9
W--> 166     Gly Cys Xaa Xaa Cys Gly Gly Cys Gly
167         1           5
169 <210> SEQ ID NO: 10
170 <211> LENGTH: 28
171 <212> TYPE: PRT
172 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
175     binding protein
176 <221> NAME/KEY: BINDING
177 <222> LOCATION: (1)..(28)
178 <400> SEQUENCE: 10
179     Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Asp Arg Ser Ser Leu
180         1           5           10           15
181     Thr Arg His Thr Arg Thr His Thr Gly Glu Lys Pro
182         20          25
184 <210> SEQ ID NO: 11
185 <211> LENGTH: 28
186 <212> TYPE: PRT
187 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
190     binding protein
191 <221> NAME/KEY: BINDING
192 <222> LOCATION: (1)..(28)
193 <400> SEQUENCE: 11
194     Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Asp Arg Ser His Leu
195         1           5           10           15
196     Thr Arg His Thr Arg Thr His Thr Gly Glu Lys Pro
197         20          25
199 <210> SEQ ID NO: 12
200 <211> LENGTH: 27
201 <212> TYPE: PRT
202 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
205     binding protein
206 <221> NAME/KEY: BINDING

```

*same
errr*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/424,487A

DATE: 03/28/2001
TIME: 15:24:58

Input Set : N:\Crf3\Refhold\I424487A.raw
Output Set: N:\CRF3\03282001\I424487A.raw

207 <222> LOCATION: (1)..(27)
208 <400> SEQUENCE: 12
209 Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Asp Arg Ser Asn Leu
210 1 5 10 15
211 Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
212 20 25
214 <210> SEQ ID NO: 13
215 <211> LENGTH: 9
216 <212> TYPE: PRT
217 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
220 binding protein
221 <221> NAME/KEY: BINDING
222 <222> LOCATION: (1)..(9)
223 <400> SEQUENCE: 13
224 Ala Gly Ala Gly Ala Gly Cys Thr Cys
225 1 5
227 <210> SEQ ID NO: 14
228 <211> LENGTH: 8
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: 8bp
233 palindromic sequence which is bound and cleaved by
234 the restriction endonuclease NotI
235 <221> NAME/KEY: BINDING
236 <222> LOCATION: (1)..(8)
237 <400> SEQUENCE: 14
238 Gly Cys Gly Gly Cys Cys Gly Cys
239 1 5
241 <210> SEQ ID NO: 15
242 <211> LENGTH: 9
243 <212> TYPE: PRT
244 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: zinc finger
247 binding protein
248 <221> NAME/KEY: BINDING
249 <222> LOCATION: (1)..(9)
250 <400> SEQUENCE: 15
251 Gly Cys Gly Gly Cys Cys Gly Cys Gly
252 1 5
254 <210> SEQ ID NO: 16
255 <211> LENGTH: 8
256 <212> TYPE: PRT
257 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Description of Artificial Sequence: NotI

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/424,487A

DATE: 03/28/2001
TIME: 15:24:59

Input Set : N:\Crf3\Refhold\I424487A.raw
Output Set: N:\CRF3\03282001\I424487A.raw

L:6 M:270 C: Current Application Number differs, Wrong Format

L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9